Amendments to the Claims

The listing of claims will replace all prior versions, and listings of claims in the application.

1. **(currently amended)** An isolated ~~nucleic acid~~ promoter sequence comprising a sequence as set forth between nucleotide positions 372 to 460 of SEQ ID NO:1.

2. **(currently amended)** The isolated ~~nucleic acid~~ promoter sequence of claim 1, wherein said sequence is selected from the group consisting of:

a) 372 to 461 of SEQ ID NO:1;

b) 372 to 522 of SEQ ID NO:1;

c) 309 to 460 of SEQ ID NO:1;

d) 309 to 461 of SEQ ID NO:1;

e) 309 to 522 of SEQ ID NO:1;

f) 207 to 460 of SEQ ID NO:1;

g) 207 to 461 of SEQ ID NO:1;

h) 207 to 522 of SEQ ID NO:1;

i) 95 to 460 of SEQ ID NO:1;

j) 95 to 461 of SEQ ID NO:1;

k) 95 to 522 of SEQ ID NO:1;

l) 28 to 460 of SEQ ID NO:1;

m) 28 to 461 of SEQ ID NO:1;

n) 28 to 522 of SEQ ID NO:1;

o) 1 to 460 of SEQ ID NO:1;

p) 1 to 461 of SEQ ID NO:1; and

q) 1 to 522 of SEQ ID NO:1.

3. (original) A vector comprising the sequence of claim 1.

4. (original) A vector comprising the sequence of claim 2.

5. (original) A cell comprising the vector of claim 3.

6. (original) A cell comprising the vector of claim 4.

7. **(currently amended)** A method of modulating the transcription of a heterologous sequence in a prostate cell, comprising: a) joining of said heterologous sequence downstream of said sequence of claim 1, so as to subject said heterologous sequence to the control of said promoter sequence; and b) assessing the level of transcription of said heterologous sequence.

8. **(currently amended)** A method of modulating an expression of a transcript in a prostate cancer cell, comprising an administration in said cell of an ~~agent~~ antisense molecule capable of modulating a transcriptional activity of said sequence of claim 1.

9. **(currently amended)** A method of identifying an agent which modulates an expression of a transcript in a prostate cell, comprising an ~~assesment~~ assessment of a transcriptional activity of ~~said~~ a promoter sequence ~~of claim 1,~~ which comprises a sequence as set forth between nucleotide positions 372 to 460 of SEQ ID NO:1, in ~~a~~ the presence, versus ~~an~~ the absence of a candidate compound, wherein an agent which modulates said transcriptional activity of said promoter sequence is selected when said transcriptional activity is significantly different in the presence of said compound, as compared to in the absence thereof.

10. (original) The method of claim 9, wherein said prostate cell is a prostate cancer cell.

11. **(currently amended)** The vector of claim 3, further comprising a heterologous sequence operably linked to said promoter sequence, wherein said heterologous sequence is selected from a sequence which encodes a reporter gene and a therapeutic sequence.

12. **(currently amended)** ~~The~~A vector ~~of claim 11~~ comprising a promoter sequence as set forth between nucleotide positions 372 to 460 of SEQ ID NO:1, operably linked to a heterologous therapeutic sequence, wherein an expression of said therapeutic sequence inhibits the growth or kills a cell in which it is expressed.

13. **(currently amended)** The vector of claim ~~11~~12, wherein said therapeutic sequence is a suicide gene.

14. (original) The vector of claim 13, further comprising an enhancer element.

15. (original) A method for diagnosing prostate cancer or a predisposition thereto in a nucleic acid prostatic sample of a patient comprising assessing in said sample, the promoter activity of said promoter sequence of claim 1, wherein an active state of said promoter sequence, as compared to an inactive state thereof, indicates a cancerous state of said prostatic sample or a predisposition of said sample to develop into a cancerous state.